

CLAIM AMENDMENTS

Claims 1 to 27 (canceled)

Claim 28 (Currently Amended)

An isolated nucleic acid ~~specific to mycobacteria of M.tuberculosis complex~~ having a nucleotide sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 29 (Currently Amended)

An isolated nucleic acid ~~specific to mycobacteria of M.tuberculosis complex~~ having a nucleotide sequence selected from the group consisting of SEQ ID No: 1 and the complement of SEQ ID No: 1.

Claim 30 (Currently Amended)

An isolated nucleic acid ~~specific to mycobacteria of M.tuberculosis complex which mycobacteria is different from BCG, whereas said nucleic acid has~~ having a nucleotide sequence selected from the group consisting of SEQ ID No: 2 and the complement of SEQ ID No: 2.

Claim 31 (Previously Presented)

A cloning or expression vector containing a nucleic acid sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 32 (previously presented)

A vector of claim 31 which is a plasmid selected from the group consisting of pRegX3Bcl and pRegX3Mt1 deposited at CNCM under Nos. I-1765 and I-1766, respectively.

Claim 33 (Canceled)

Claim 34 (Previously Presented)

A nucleotide probe or nucleotide primer comprising 24 consecutive nucleotides selected from a sequence selected from the group consisting of SEQ ID No:1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 35 (Currently Amended)

A nucleotide probe or nucleotide primer that hybridizes at 68°C in a 5xSSC hybridization buffer with one of the sequences comprising a sequence selected from the

group consisting of sequence SEQ ID No: 1, or the complement of SEQ ID No: 1, or their corresponding RNA sequences and their corresponding gene[s], and that contains a maximum of 21 base pairs.

Claim 36 (Currently Amended)

A nucleotide probe or nucleotide primer that hybridizes at 68°C in a 5xSSC hybridization buffer with one of the sequences having a sequence comprising two successive sequences SEQ ID No: 1 followed by a sequence SEQ ID No: 2 or their corresponding RNA sequences or their corresponding gene, and that contains a maximum of 21 base pairs.

Claim 37 (Currently Amended)

A nucleotide probe for detection of specific sequences of nucleic acids of M.tuberculosis complex other than BCG wherein said probe that consists of 21 base pairs having a sequence of a region of sequence SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 or the complement of said region.

Claim 38 (Currently Amended)

A nucleotide probe for detection of specific sequences of nucleic acids of *M. tuberculosis* complex other than BCG comprising a sequence composed of nucleotides in positions 31 to 51 of SEQ ID No: 2 or the complement of said sequence.

Claim 39 (Canceled)

Claim 40 (Currently Amended)

A nucleotide probe of claim 37 comprising the sequence SEQ ID No: 2 or the complement of SEQ ID No: 2.

Claim 41 (Currently Amended)

A nucleotide probe or nucleotide primer that hybridizes at 68°C in a 5xSSC hybridization buffer with labeled by digoxigenin comprising one of the sequences selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2, their corresponding RNA sequences or and their corresponding gene[s], and that contains a maximum of 21 base pairs, which is labeled by dioxygenin.

Claim 42 (Canceled)

Claim 43 (Canceled)

Claim 44 (Currently Amended)

A nucleotide primer pair ~~of claim 42 comprising the a~~ pair of primers 5' GCGCGAGAGCCGAACTGC3' (SEQ ID No: 4) and 5' GCGCAGCAGAACGTCAGC3' (SEQ ID No: 5).

Claims 45 and 46 (canceled)

Claim 47 (Currently Amended)

A method of detecting a mycobacteria stain strain of M. tuberculosis complex in a biological sample comprising

(1) contacting the biological sample to a pair of primers
5' GCGCGAGAGCCGAACTGC3' (SEQ ID No: 4) and
5' GCGCAGCAGAACGTCAGC3' (SEQ ID No: 5) wherein one primer comprises the nucleotide sequence of sequences adjacent to the ~~senX3-regX3~~ region in the 3' of ~~senX3~~ region and the other primer comprises the nucleotide sequence of sequences adjacent to the ~~senX3-regX3~~ region in the 5' of ~~regX3~~ region under conditions to effect hybridization of the primers to a nucleotide sequence ~~the specific nucleic acids~~ of mycobacteria strains of M. tuberculosis complex;

(2) effecting amplification of the said nucleotide sequence ~~nucleic acids~~;

(3) contacting the biological sample containing said nucleotide sequences amplified from step (2) with a nucleotide probe that hybridizes at 68 °C in a 5xSSC hybridization buffer with one of the sequences that comprises a sequence selected from the group consisting of SEQ ID No: 1, or sequence SEQ ID No: 2, or the complement of SEQ ID No: 1, or and the complement of SEQ ID No: 2, or one of their corresponding RNA sequences or one of their corresponding gene[s], or a sequence of two successive sequence of SEQ ID No: 1 followed by SEQ ID No: 2, and that contains a maximum of 21 base pairs under conditions for formation of hybridization complexes between the said probe and said nucleotide sequences amplified sequences from step (2) of nucleic acids; and

(4) detecting if any hybridization complexes are present, which complexes indicate the a presence of a mycobacteria strain of *M. tuberculosis* complex.

Claim 48 (Canceled)

Claim 49 (Currently Amended)

The method of claim 47 wherein the nucleotide probe comprises a region of SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 or the complement of said region a

sequence composed of nucleotides in positions 31 to 51 of SEQ ID No: 2 or the complement of said sequence.

Claim 50 (previously presented)

The method of claim 49 effected upon immunodeficient humans to differentiate an infection by BCG from an infection by a virulent mycobacterium of M. tuberculosis complex.

Claim 51 (previously presented)

The method of claim 50 wherein the human is infected with HIV.

Claim 52 (Currently Amended)

A method of identifying groups of mycobacteria belonging to a M. tuberculosis complex comprising

(1) contacting ~~the~~^a DNA of previously extracted strains of the M. tuberculosis complex with a nucleotide primer pair comprising a pair of primers

5' GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and

5' GCGCAGCAGAACGTCAGC3' (SEQ ID No: 5) ~~of claims 35 and 42~~

under conditions permitting a specific hybridization of the primers respectively 56 base pairs upstream and 62 base pairs downstream of ~~with one of the sequences of claim 28~~

a sequence selected from the group consisting of SEQ ID No:
1, SEQ ID No: 2, the complement of SEQ ID No: 1 and the
complement of SEQ ID No: 2, to obtain amplification
products and

(2) measuring ~~the~~^a length of the amplification
products obtained from step (1).

Claim 53 (Canceled)

Claim 54 (Currently Amended)

A kit for in vitro identification of strains of mycobacteria of a ~~the~~ M. tuberculosis complex in a biological sample comprising (1) a primer pair for amplification of a specific nucleotide sequence of mycobacteria of M. tuberculosis complex, one primer consisting of the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3' of senX3 region and the other primer consisting of the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' of regX3 region a pair of primers 5' GCGCGAGAGCCGAACTGC3' (SEQ ID No: 4) and 5' GCGCAGCAGAACGTCAGC3' (SEQ ID No: 5).

Claim 55 (Currently Amended)

A method of detection and of differential diagnosis of BCG and the members of M. tuberculosis complex in a biological sample comprising:

(1) contacting the biological sample to a nucleotide primer pair comprising a pair of primers
5' GCGCGAGAGCCCCGAAGTC3' (SEQ ID No: 4) and
5' GCGCAGCAGAACGTCAGC3' (SEQ ID No: 5) for amplification of a specific nucleotide sequence of mycobacteria of M. tuberculosis complex, one primer comprising the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3' of senX3 region and the other primer comprising the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' of regX3 region under conditions to effect hybridization of the primers to said nucleotide sequence the specific nucleic acids of mycobacteria strains of M. tuberculosis complex;

(2) effecting amplification of the said nucleotide sequence nucleic acids;

(3) contacting the biological sample containing said nucleotide sequence amplified from step (2) with a nucleotide probe of two successive sequences SEQ ID No: 1 followed by a sequence SEQ ID No: 2 under conditions for formation of hybridization complexes between the said probe

and said nucleotide amplified sequences amplified from step
(2) of nucleic acids;

(4) detecting any first hybridization complexes present; and

(5) determining if said first hybridization complexes are also capable of forming second hybridization complexes with a nucleotide probe for detection of ~~specifie~~ sequences of nucleic acids of M. tuberculosis complex other than BCG comprising a ~~region of sequence SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 sequence composed of~~ nucleotides in positions 31 to 51 of SEQ ID No:2, or the complement of said sequence region, ~~the-a~~ presence of said second hybridization complexes being indicative of ~~the-a~~ presence of a M. tuberculosis strain different from BCG and ~~the-a~~ presence of said first hybridization complexes uniquely being indicative of the BCG.